

SEQUENCE LISTING

<110> WU, TZZY-CHOOU
HUNG, CHIEN, FU

<120> ANTI-CANCER DNA VACCINE EMPLOYING PLASMIDS ENCODING
SIGNAL SEQUENCE, MUTANT ONCOPROTEIN ANTIGEN, AND HEAT
SHOCK PROTEIN

<130> JHV-050.01 (19546-5001)

<140> 10/555,669

<141> 2004-05-05

<150> PCT/US04/013756

<151> 2004-05-05

<150> 60/467,602

<151> 2003-05-05

<160> 20

<170> PatentIn Ver. 3.3

<210> 1

<211> 297

<212> DNA

<213> Human papillomavirus

<220>

<221> CDS

<222> (1)..(297)

<400> 1

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1				5					10					15		

cca	gag	aca	act	gat	ctc	tac	tgt	tat	gag	caa	tta	aat	gac	agc	tca	96
Pro	Glu	Thr	Thr	Asp	Leu	Tyr	Cys	Tyr	Glu	Gln	Leu	Asn	Asp	Ser	Ser	
			20					25					30			

gag	gag	gag	gat	gaa	ata	gat	ggt	cca	gct	gga	caa	gca	gaa	ccg	gac	144
Glu	Glu	Glu	Asp	Glu	Ile	Asp	Gly	Pro	Ala	Gly	Gln	Ala	Glu	Pro	Asp	
		35					40					45				

aga	gcc	cat	tac	aat	att	gta	acc	ttt	tgt	tgc	aag	tgt	gac	tct	acg	192
Arg	Ala	His	Tyr	Asn	Ile	Val	Thr	Phe	Cys	Cys	Lys	Cys	Asp	Ser	Thr	
	50					55					60					

ctt	cgg	ttg	tgc	gta	caa	agc	aca	cac	gta	gac	att	cgt	act	ttg	gaa	240
Leu	Arg	Leu	Cys	Val	Gln	Ser	Thr	His	Val	Asp	Ile	Arg	Thr	Leu	Glu	
65					70				75					80		

gac	ctg	tta	atg	ggc	aca	cta	gga	att	gtg	tgc	ccc	atc	tgt	tct	cag	288
Asp	Leu	Leu	Met	Gly	Thr	Leu	Gly	Ile	Val	Cys	Pro	Ile	Cys	Ser	Gln	
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gat aag ctt
Asp Lys Leu

297

<210> 2
<211> 99
<212> PRT
<213> Human papillomavirus

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Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
1 5 10 15
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
20 25 30
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
35 40 45
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
50 55 60
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65 70 75 80
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
85 90 95
Asp Lys Leu

<210> 3
<211> 98
<212> PRT
<213> Human papillomavirus

<400> 3
Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
1 5 10 15
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
20 25 30
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
35 40 45
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
50 55 60
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65 70 75 80
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
85 90 95
Lys Pro

<210> 4
 <211> 158
 <212> PRT
 <213> Human papillomavirus

<400> 4
 Met His Gln Lys Arg Thr Ala Met Phe Gln Asp Pro Gln Glu Arg Pro
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 Arg Lys Leu Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp
 20 25 30
 Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu
 35 40 45
 Val Tyr Asp Phe Ala Phe Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly
 50 55 60
 Asn Pro Tyr Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile
 65 70 75 80
 Ser Glu Tyr Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu
 85 90 95
 Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn
 100 105 110
 Cys Gln Lys Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp Lys
 115 120 125
 Lys Gln Arg Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys Met
 130 135 140
 Ser Cys Cys Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Leu
 145 150 155

<210> 5
 <211> 151
 <212> PRT
 <213> Human papillomavirus

<400> 5
 Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu Pro Gln Leu Cys
 1 5 10 15
 Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val Tyr
 20 25 30
 Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe Arg
 35 40 45
 Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys Asp
 50 55 60

Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr Arg His Tyr Cys
 65 70 75 80
 Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro Leu
 85 90 95
 Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro Leu Cys Pro
 100 105 110
 Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn Ile
 115 120 125
 Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser Arg
 130 135 140
 Thr Arg Arg Glu Thr Gln Leu
 145 150

<210> 6
 <211> 378
 <212> DNA
 <213> Human papillomavirus

<400> 6
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 ggcgcctcag cactctttga ggatctaatac atgcatggag atacacctac attgcatgaa 120
 tatatgtag atttgcaacc agagacaact gatctctact gttatgagca attaaatgac 180
 agctcagagg aggaggatga aatagatggt ccagctggac aagcagaacc ggacagagcc 240
 cattacaata ttgtaacctt ttgttgcaag tgtgactcta cgcttcggtt gtgcgtacaa 300
 agcacacacg tagacattcg tactttggaa gacctgttaa tgggcacact aggaattgtg 360
 tgccccatct gttctcaa 378

<210> 7
 <211> 127
 <212> PRT
 <213> Human papillomavirus

<400> 7
 Met Ala Ala Pro Gly Ala Arg Arg Pro Leu Leu Leu Leu Leu Ala
 1 5 10 15
 Gly Leu Ala His Gly Ala Ser Ala Leu Phe Glu Asp Leu Ile Met His
 20 25 30
 Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln Pro Glu
 35 40 45
 Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser Glu Glu
 50 55 60
 Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala
 65 70 75 80
 His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr Leu Arg
 85 90 95

Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu Asp Leu
 100 105 110

Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln Pro
 115 120 125

<210> 8
 <211> 90
 <212> DNA
 <213> Human papillomavirus

<400> 8
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 ggcgccctcag cactctttga ggatctaata 90

<210> 9
 <211> 1878
 <212> DNA
 <213> Mycobacterium tuberculosis

<400> 9
 atggctcgtg cggtcgggat cgacctcggg accaccaact ccgtcgtctc ggttctggaa 60
 ggtggcgacc cggtcgtcgt cgccaactcc gaggggtcca ggaccacccc gtcaattgtc 120
 gcgttcgccc gcaacggtga ggtgctggtc ggccagcccg ccaagaacca ggcagtgacc 180
 aacgtcgatc gcaccgtgcg ctccgtcaag cgacacatgg gcagcgactg gtccatagag 240
 attgacggca agaaatacac cgcgcccggag atcagcgccc gcattctgat gaagctgaag 300
 cgcgaccccg aggcctacct cggtagggac attaccgacg cggttatcac gacgcccgcg 360
 tacttcaatg acgcccagcg tcaggccacc aaggacgccc gccagatcgc cggcctcaac 420
 gtgctgcgga tcgtcaacga gccgaccgcg gccgcgctgg cctacggcct cgacaagggc 480
 gagaaggagc agcgaatcct ggtcttcgac ttgggtggtg gcactttcga cgtttccctg 540
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 ggcgacgact gggaccagcg ggtcgtcgat tggctggtgg acaagttaa gggcaccagc 660
 ggcacgatc tgaccaagga caagatggcg atgcagcggc tgcgggaagc cgcgagag 720
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 gacgcccaga agaaccggtt gttcttagac gagcagctga cccgcgcgga gttccaacgg 840
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 ggcatttcgg tgcgagat cgatcacgtt gtgctcgtgg gtggttcgac ccggtgccc 960
 gcggtgaccg atctggtcaa ggaactcacc ggcggcaagg aaccaacaa gggcgtcaac 1020
 cccgatgagg ttgtcgcggt gggagccgct ctgcaggccg gcgtcctcaa gggcgaggtg 1080
 aaagacgttc tgctgcttga tgttaccgct ctgagcctgg gtatcgagac caagggcggg 1140
 gtgatgacca ggctcatcga gcgcaacacc acgatcccca ccaagcggtc ggagactttc 1200
 accaccgccc acgacaacca accgtcggtg cagatccagg tctatcaggg ggagcgtgag 1260
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 cgggggattc cgcagatcga ggtcactttc gacatcgacg ccaacggcat tgtgcacgtc 1380
 accgccaagg acaagggcac cggcaaggag aacacgatcc gaatccagga aggtcgggc 1440
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 cgcaagcgtc gcgaggaggc cgatgttcgt aatcaagccc agacattggt ctaccagacg 1560
 gagaagttcg tcaaagaaca gcgtgaggcc gaggggtggt cgaaggtacc tgaagacacg 1620
 ctgaacaagg ttgatgccgc ggtggcggaa gcgaaggcgg cacttgccgg atcgatatt 1680
 tcggccatca agtcggcgat ggagaagctg ggccaggagt cgcaggctct ggggcaagcg 1740
 atctacgaag cagctcaggc tcgctcacag gccactggcg ctgcccaccc cggcgcgag 1800
 ccggggcggtg cccaccccgg ctccgctgat gacgttgtgg acgcggaggt ggtcgacgac 1860
 ggccgggagg ccaagtga 1878

<210> 10

<211> 625

<212> PRT

<213> Mycobacterium tuberculosis

<400> 10

Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
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Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
 20 25 30

Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
 35 40 45

Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
 50 55 60

Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
 65 70 75 80

Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu
 85 90 95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
 100 105 110

Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
 115 120 125

Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
 130 135 140

Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
 145 150 155 160

Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
 165 170 175

Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
 180 185 190

Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
 195 200 205

Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Ile Asp Leu
 210 215 220

Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
 225 230 235 240

Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
 245 250 255

Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
 260 265 270

Leu	Thr	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Asp	Arg	275	280	285
Thr	Arg	Lys	Pro	Phe	Gln	Ser	Val	Ile	Ala	Asp	Thr	Gly	Ile	Ser	Val	290	295	300
Ser	Glu	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro	310	315	320
Ala	Val	Thr	Asp	Leu	Val	Lys	Glu	Leu	Thr	Gly	Gly	Lys	Glu	Pro	Asn	325	330	335
Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	Leu	Gln	340	345	350
Ala	Gly	Val	Leu	Lys	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val	355	360	365
Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	Thr	Arg	370	375	380
Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	Thr	Phe	385	390	395
Thr	Thr	Ala	Asp	Asp	Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln	Val	Tyr	Gln	405	410	415
Gly	Glu	Arg	Glu	Ile	Ala	Ala	His	Asn	Lys	Leu	Leu	Gly	Ser	Phe	Glu	420	425	430
Leu	Thr	Gly	Ile	Pro	Pro	Ala	Pro	Arg	Gly	Ile	Pro	Gln	Ile	Glu	Val	435	440	445
Thr	Phe	Asp	Ile	Asp	Ala	Asn	Gly	Ile	Val	His	Val	Thr	Ala	Lys	Asp	450	455	460
Lys	Gly	Thr	Gly	Lys	Glu	Asn	Thr	Ile	Arg	Ile	Gln	Glu	Gly	Ser	Gly	465	470	475
Leu	Ser	Lys	Glu	Asp	Ile	Asp	Arg	Met	Ile	Lys	Asp	Ala	Glu	Ala	His	485	490	495
Ala	Glu	Glu	Asp	Arg	Lys	Arg	Arg	Glu	Glu	Ala	Asp	Val	Arg	Asn	Gln	500	505	510
Ala	Glu	Thr	Leu	Val	Tyr	Gln	Thr	Glu	Lys	Phe	Val	Lys	Glu	Gln	Arg	515	520	525
Glu	Ala	Glu	Gly	Gly	Ser	Lys	Val	Pro	Glu	Asp	Thr	Leu	Asn	Lys	Val	530	535	540
Asp	Ala	Ala	Val	Ala	Glu	Ala	Lys	Ala	Ala	Leu	Gly	Gly	Ser	Asp	Ile	545	550	555
Ser	Ala	Ile	Lys	Ser	Ala	Met	Glu	Lys	Leu	Gly	Gln	Glu	Ser	Gln	Ala	565	570	575

Leu Gly Gln Ala Ile Tyr Glu Ala Ala Gln Ala Ala Ser Gln Ala Thr
 580 585 590

Gly Ala Ala His Pro Gly Gly Glu Pro Gly Gly Ala His Pro Gly Ser
 595 600 605

Ala Asp Asp Val Val Asp Ala Glu Val Val Asp Asp Gly Arg Glu Ala
 610 615 620

Lys
 625

<210> 11
 <211> 2104
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(2103)

<220>
 <223> Description of Artificial Sequence: Synthetic
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 1 5 10 15

cca gag aca act gat ctc tac tgt tat gag caa tta aat gac agc tca 96
 Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
 20 25 30

gag gag gag gat gaa ata gat ggt cca gct gga caa gca gaa ccg gac 144
 Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
 35 40 45

aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt gac tct acg 192
 Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
 50 55 60

ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt act ttg gaa 240
 Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
 65 70 75 80

gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc tgt tct caa 288
 Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
 85 90 95

gga tcc atg gct cgt gcg gtc ggg atc gac ctc ggg acc acc aac tcc 336
 Gly Ser Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser
 100 105 110

gtc gtc tcg gtt ctg gaa ggt ggc gac ccg gtc gtc gtc gcc aac tcc 384
 Val Val Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser
 115 120 125

gag ggc tcc agg acc acc ccg tca att gtc gcg ttc gcc cgc aac ggt	432
Glu Gly Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly	
130 135 140	
gag gtg ctg gtc ggc cag ccc gcc aag aac cag gca gtg acc aac gtc	480
Glu Val Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val	
145 150 155 160	
gat cgc acc gtg cgc tcg gtc aag cga cac atg ggc agc gac tgg tcc	528
Asp Arg Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser	
165 170 175	
ata gag att gac ggc aag aaa tac acc gcg ccg gag atc agc gcc cgc	576
Ile Glu Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg	
180 185 190	
att ctg atg aag ctg aag cgc gac gcc gag gcc tac ctc ggt gag gac	624
Ile Leu Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp	
195 200 205	
att acc gac gcg gtt atc acg acg ccc gcc tac ttc aat gac gcc cag	672
Ile Thr Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln	
210 215 220	
cgt cag gcc acc aag gac gcc ggc cag atc gcc ggc ctc aac gtg ctg	720
Arg Gln Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu	
225 230 235 240	
cgg atc gtc aac gag ccg acc gcg gcc gcg ctg gcc tac ggc ctc gac	768
Arg Ile Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp	
245 250 255	
aag ggc gag aag gag cag cga atc ctg gtc ttc gac ttg ggt ggt ggc	816
Lys Gly Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly	
260 265 270	
act ttc gac gtt tcc ctg ctg gag atc ggc gag ggt gtg gtt gag gtc	864
Thr Phe Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val	
275 280 285	
cgt gcc act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag	912
Arg Ala Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln	
290 295 300	
cgg gtc gtc gat tgg ctg gtg gac aag ttc aag ggc acc agc ggc atc	960
Arg Val Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Ile	
305 310 315 320	
gat ctg acc aag gac aag atg gcg atg cag cgg ctg cgg gaa gcc gcc	1008
Asp Leu Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala	
325 330 335	
gag aag gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac	1056
Glu Lys Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn	
340 345 350	

ctg	ccc	tac	atc	acc	gtc	gac	gcc	gac	aag	aac	ccg	ttg	ttc	tta	gac	1104
Leu	Pro	Tyr	Ile	Thr	Val	Asp	Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	
		355					360					365				
gag	cag	ctg	acc	cgc	gcg	gag	ttc	caa	cgg	atc	act	cag	gac	ctg	ctg	1152
Glu	Gln	Leu	Thr	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	
	370					375					380					
gac	cgc	act	cgc	aag	ccg	ttc	cag	tcg	gtg	atc	gct	gac	acc	ggc	att	1200
Asp	Arg	Thr	Arg	Lys	Pro	Phe	Gln	Ser	Val	Ile	Ala	Asp	Thr	Gly	Ile	
385					390					395					400	
tcg	gtg	tcg	gag	atc	gat	cac	gtt	gtg	ctc	gtg	ggg	ggg	tcg	acc	cgg	1248
Ser	Val	Ser	Glu	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	
				405					410					415		
atg	ccc	gcg	gtg	acc	gat	ctg	gtc	aag	gaa	ctc	acc	ggc	ggc	aag	gaa	1296
Met	Pro	Ala	Val	Thr	Asp	Leu	Val	Lys	Glu	Leu	Thr	Gly	Gly	Lys	Glu	
		420						425					430			
ccc	aac	aag	ggc	gtc	aac	ccc	gat	gag	gtt	gtc	gcg	gtg	gga	gcc	gct	1344
Pro	Asn	Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	
		435					440					445				
ctg	cag	gcc	ggc	gtc	ctc	aag	ggc	gag	gtg	aaa	gac	gtt	ctg	ctg	ctt	1392
Leu	Gln	Ala	Gly	Val	Leu	Lys	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	
	450					455					460					
gat	gtt	acc	ccg	ctg	agc	ctg	ggg	atc	gag	acc	aag	ggc	ggg	gtg	atg	1440
Asp	Val	Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	
465					470					475					480	
acc	agg	ctc	atc	gag	cgc	aac	acc	acg	atc	ccc	acc	aag	cgg	tcg	gag	1488
Thr	Arg	Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	
				485					490					495		
act	ttc	acc	acc	gcc	gac	gac	aac	caa	ccg	tcg	gtg	cag	atc	cag	gtc	1536
Thr	Phe	Thr	Thr	Ala	Asp	Asp	Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln	Val	
			500					505					510			
tat	cag	ggg	gag	cgt	gag	atc	gcc	gcg	cac	aac	aag	ttg	ctc	ggg	tcc	1584
Tyr	Gln	Gly	Glu	Arg	Glu	Ile	Ala	Ala	His	Asn	Lys	Leu	Leu	Gly	Ser	
		515					520					525				
ttc	gag	ctg	acc	ggc	atc	ccg	ccg	gcg	ccg	cgg	ggg	att	ccg	cag	atc	1632
Phe	Glu	Leu	Thr	Gly	Ile	Pro	Pro	Ala	Pro	Arg	Gly	Ile	Pro	Gln	Ile	
	530					535					540					
gag	gtc	act	ttc	gac	atc	gac	gcc	aac	ggc	att	gtg	cac	gtc	acc	gcc	1680
Glu	Val	Thr	Phe	Asp	Ile	Asp	Ala	Asn	Gly	Ile	Val	His	Val	Thr	Ala	
545					550					555					560	
aag	gac	aag	ggc	acc	ggc	aag	gag	aac	acg	atc	cga	atc	cag	gaa	ggc	1728
Lys	Asp	Lys	Gly	Thr	Gly	Lys	Glu	Asn	Thr	Ile	Arg	Ile	Gln	Glu	Gly	
				565					570					575		

tcg ggc ctg tcc aag gaa gac att gac cgc atg atc aag gac gcc gaa	1776
Ser Gly Leu Ser Lys Glu Asp Ile Asp Arg Met Ile Lys Asp Ala Glu	
580 585 590	
gcg cac gcc gag gag gat cgc aag cgt cgc gag gag gcc gat gtt cgt	1824
Ala His Ala Glu Glu Asp Arg Lys Arg Arg Glu Glu Ala Asp Val Arg	
595 600 605	
aat caa gcc gag aca ttg gtc tac cag acg gag aag ttc gtc aaa gaa	1872
Asn Gln Ala Glu Thr Leu Val Tyr Gln Thr Glu Lys Phe Val Lys Glu	
610 615 620	
cag cgt gag gcc gag ggt ggt tcg aag gta cct gaa gac acg ctg aac	1920
Gln Arg Glu Ala Glu Gly Gly Ser Lys Val Pro Glu Asp Thr Leu Asn	
625 630 635 640	
aag gtt gat gcc gcg gtg gcg gaa gcg aag gcg gca ctt ggc gga tcg	1968
Lys Val Asp Ala Ala Val Ala Glu Ala Lys Ala Ala Leu Gly Gly Ser	
645 650 655	
gat att tcg gcc atc aag tcg gcg atg gag aag ctg ggc cag gag tcg	2016
Asp Ile Ser Ala Ile Lys Ser Ala Met Glu Lys Leu Gly Gln Glu Ser	
660 665 670	
cag gct ctg ggg caa gcg atc tac gaa gca gct cag gct gcg tca cag	2064
Gln Ala Leu Gly Gln Ala Ile Tyr Glu Ala Ala Gln Ala Ala Ser Gln	
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690 695 700	

<210> 12

<211> 701

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<400> 12

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35 40 45	
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr	
50 55 60	
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu	
65 70 75 80	

Asp	Leu	Leu	Met	Gly	Thr	Leu	Gly	Ile	Val	Cys	Pro	Ile	Cys	Ser	Gln	85	90	95	
Gly	Ser	Met	Ala	Arg	Ala	Val	Gly	Ile	Asp	Leu	Gly	Thr	Thr	Asn	Ser	100	105	110	
Val	Val	Ser	Val	Leu	Glu	Gly	Gly	Asp	Pro	Val	Val	Val	Ala	Asn	Ser	115	120	125	
Glu	Gly	Ser	Arg	Thr	Thr	Pro	Ser	Ile	Val	Ala	Phe	Ala	Arg	Asn	Gly	130	135	140	
Glu	Val	Leu	Val	Gly	Gln	Pro	Ala	Lys	Asn	Gln	Ala	Val	Thr	Asn	Val	145	150	155	160
Asp	Arg	Thr	Val	Arg	Ser	Val	Lys	Arg	His	Met	Gly	Ser	Asp	Trp	Ser	165	170	175	
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Lys	Gly	Glu	Lys	Glu	Gln	Arg	Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	260	265	270	
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Asp	Leu	Thr	Lys	Asp	Lys	Met	Ala	Met	Gln	Arg	Leu	Arg	Glu	Ala	Ala	325	330	335	
Glu	Lys	Ala	Lys	Ile	Glu	Leu	Ser	Ser	Ser	Gln	Ser	Thr	Ser	Ile	Asn	340	345	350	
Leu	Pro	Tyr	Ile	Thr	Val	Asp	Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	355	360	365	
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Thr	Arg	Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	485	490	495	
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Lys	Asp	Lys	Gly	Thr	Gly	Lys	Glu	Asn	Thr	Ile	Arg	Ile	Gln	Glu	Gly	565	570	575	
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Ala	His	Ala	Glu	Glu	Asp	Arg	Lys	Arg	Arg	Glu	Glu	Ala	Asp	Val	Arg	595	600	605	
Asn	Gln	Ala	Glu	Thr	Leu	Val	Tyr	Gln	Thr	Glu	Lys	Phe	Val	Lys	Glu	610	615	620	
Gln	Arg	Glu	Ala	Glu	Gly	Gly	Ser	Lys	Val	Pro	Glu	Asp	Thr	Leu	Asn	625	630	635	640
Lys	Val	Asp	Ala	Ala	Val	Ala	Glu	Ala	Lys	Ala	Ala	Leu	Gly	Gly	Ser	645	650	655	
Asp	Ile	Ser	Ala	Ile	Lys	Ser	Ala	Met	Glu	Lys	Leu	Gly	Gln	Glu	Ser	660	665	670	
Gln	Ala	Leu	Gly	Gln	Ala	Ile	Tyr	Glu	Ala	Ala	Gln	Ala	Ala	Ser	Gln	675	680	685	

Ala Thr Gly Ala Ala His Pro Gly Ser Ala Asp Glu Ser
690 695 700

<210> 13
<211> 6681
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
vector

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<210> 14

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic primer

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37

<210> 15

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 15

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36

<210> 16

<211> 9

<212> PRT

<213> Human papillomavirus

<400> 16

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<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (21)

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

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21

<210> 18

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 18

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<210> 19

<211> 21

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1)..(21)

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<223> Description of Artificial Sequence: Synthetic
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<400> 19

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Leu Tyr Gly Tyr Gly Gln Leu
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21

<210> 20

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 20

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